Complex dynamics of the biological rhythms: gallbladder and heart cases

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Abstract

A theoretical analysis of the mechanisms underlying the dynamics of gallbladder and heart pulsation could clarify the question regarding the classification as chaotic of the associated behaviour, eventually related to a normal and healthy beat; this analysis is particularly relevant in view of the control of dynamics bifurcations arising in situations of disease. In this work is presented a summary of the DFA method applied to gallbladder volume data for a modest number of healthy and ill patients: the presence of signal correlation is found in both cases, but the fit shapes differ from some critical values.

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Complex systems, as observed in nature and modelled by mechanical or electrical approximations, have a dynamics characterized by dependence on many competing effects admitting multiple possible behaviours, so that the system tends to alternate among them.The task of the description of such a variegate structure relies in the research of a manifest form of coherent structure, in order to recognize a hierarchy of patterns over a wide range of time and/or length scales. Commonly comprehension of natural systems is based on highly simplified models testing linearised or tractable equations, though the intrinsic approximations of numerical methods to solve sets of differential equations have to be taken with much care, because of the unavoidable effect over the results due to the high sensitivity to approximations and to initial conditions of chaotic systems. Thus, a high level of unpredictability on the subsequent dynamics behaviour often remains, especially when studying a living system. The goal in an study of the data as well as of the model is to find a possible

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clear distinction between the normal (healthy) and the pathological cases.
We consider the pulsation of the gallbladder and of the cardiac muscle, with particular attention to the former as an example for application of the Detrended Fluctuation Analysis (DFA) method [1] to data manipulation. For the latter, an analysis of the implications of fibres geometry over the cardiac muscle is needed, in the framework of a theoretical model for heart activity assuming several pacemakers bounded to the fibres in the heart complex geometry. The methods so far adopted rely either on phenomenological models of waves propagating over the cardiac muscle seen as a membrane [4,5], either on the application of data analysis methods [3] looking for traces of chaoticity or fractality. The idea of linking the healthy heart rate to a fractal behaviour is based on [7], the ill dynamics presenting a regular inter-beat interval, a re-entrant spiral wave is observable at the very last beat of the stopping the heart together with ventricular fibrillation [2]. Let us consider how to connect fractals to gallbladder in humans. The term *fractal* is associated to a geometrical object satisfying the criteria of *self-similarity*, i.e. the existence of a sub-structure composed of sub-units resembling some statistical properties of the whole object, and *fractal dimensionality*. The test to determine if a 2-dimensional curve is self-similar consists firstly of taking a subset of the object and rescaling it to the same size of the original object, using the same magnification factor for both its width and height and, secondly, comparing the statistical properties of the rescaled object with the original object [6]. In contrast, to properly compare a subset of a time series with the original data set, we need *two* magnification factors (along the horizontal and vertical axes), since these two axes represent different physical variables.
A time-dependent process $y(t)$ (time series) is self-similar with self-similarity parameter α if

$$y(t) \equiv a^{\alpha} y\left(\frac{t}{a}\right) , \tag{1}$$

i.e. $y(t)$ has the identical probability distribution as a properly rescaled process, $a^{\alpha}y(t/a)$: a time series is rescaled on the x-axis by a factor a, $(t \to t/a)$, and on the y-axis by a^{α}, $(y \to a^{\alpha}y)$.
The method of DFA is based on this concept and permits to operate on "real-world" time series with a given procedure. For any given size of observation window, the time series is divided into subsets of independent windows of the same size. To obtain a more reliable estimation of the characteristic fluctuation at this window size, we average over all individual values of standard deviations s associated to different sets of data and obtained from these subsets, then we repeat these calculations for many different window sizes. The exponent α is estimated by fitting a line on the log-log plot of s versus the number of data n belonging to each window across the relevant range of scales. We consider stationary time series, i.e. mean, standard deviation and higher moments, correlation functions are invariant under time translation. The fractal analysis applied to physiologic time series is pursued for highly non-stationary by an integration procedure which will make the non-stationarity of the original

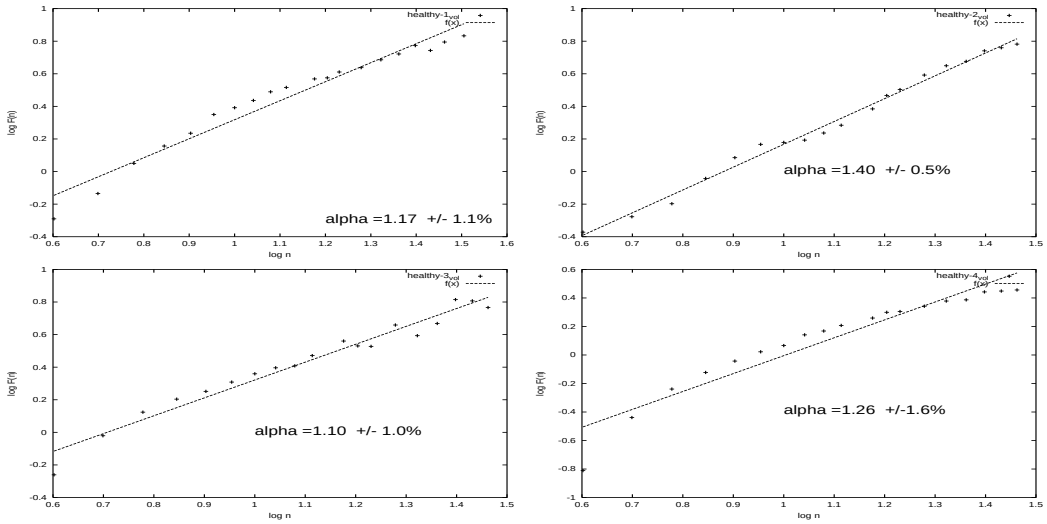

Fig. 1. Healthy behaviours – DFA of gallbladder volumes evolution with linear fit giving values of corresponding correlation parameter α.

data even more apparent. The advantages of DFA over conventional methods (e.g., spectral analysis and Hurst analysis) rely on the detection of intrinsic correlation embedded in a seemingly non-stationary time-series and on avoiding spurious detection of apparent correlation, which may be an artefact of extrinsic trends [3].The time-series of signals $B(i)$ is firstly integrated and then the trend is computed via the function $F(n)$

$$y(k) = \sum_{i=1}^{k} [B(i) - B_{ave}] \qquad F(n) = \sqrt{\frac{1}{N} \sum_{k=1}^{N} [y(k) - y_n(k)]^2} \tag{2}$$

which relates the least squares fluctuation in each box of data to the number of points belonging to that box and the correlation parameter is related to the mean square fluctuation as

$$\alpha = \frac{\ln M_y}{\ln M_x} = \frac{\ln s_2 - \ln s_1}{\ln n_2 - \ln n_1}\,, \tag{3}$$

for magnification windows along the x- and $y-$axis M_x and M_y, respectively, and standard deviations $s_{1,2}$ corresponding to boxes of dimension $n_{1,2}$, and then is computable as the slope on a log-log plot of $F(n)$ versus n. It is usually classified the level of correlation as: (i) $\alpha \in (0, 0.5)$ anticorrelation; (ii.a) $\alpha \sim 0.5$ short-term exponential correlation; (ii.b) $\alpha = 0.5$ white noise; (iii) $\alpha \in (0.5, 1)$ persistent long-range correlation; (iv.a) $\alpha > 1$ correlation, not power law; (iv.b) Brown noise. Our data has been taken through ecographic gallbladder volume evaluations of people who was known to be ill or healthy (illness related to the presence of small balls of fat in the gallbladder, viewable in the ecography, thus affecting the secretion outflow). From our results performed via the Physionet Software for DFA [1], though preliminary and for a small set of data, we see that even if there is not a sharp distinction

Healthy	α	$\pm\%$	**Ill**	α	$\pm\%$
H 1	1.17	1.1	I 1	0.92	1.2
H 2	1.40	0.5	I 2	1.87	0.5
H 3	1.10	1.0	I 3	1.03	2.2
H 4	1.26	1.6	I 4	1.35	0.7

Table 1
Computed values of the correlation factor α regarding gallbladder volume for healthy (left) and ill (right) cases with percentual error. Data set consisting of roughly 40 measurements.

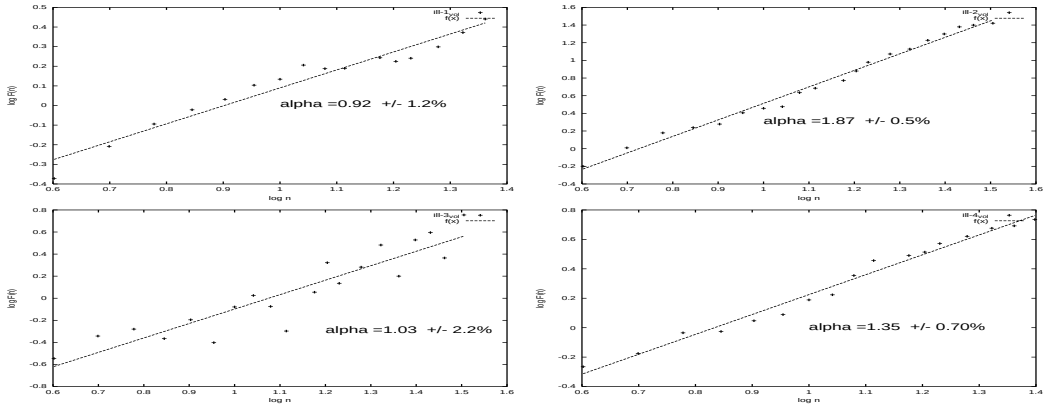

Fig. 2. Ill behaviours – DFA of gallbladder volumes evolution with linear fit giving values of corresponding correlation parameter α.

between healthy and ill situations, some of the ill patients present an α with a higher deviation from the value of unity, showing how the vibration of an obstructed gallbladder during digestion (for 40 minutes after a lunch) can be characterized even by not-power-law correlation.

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